June 23, 2004

To whom it may concern:

I am writing to express my support for the plans to sequence the Nasonia genome. Nasonia is a fascinating organism, whose study is leading to powerful new insights at the levels of development, behavior, and evolution. Sequencing its genome will not only lead to more sophisticated annotation of vertebrate and invertebrate genes, but it will also allow researchers to use Nasonia as a model system for studying the functions of genes identified in other invertebrate systems, which are not as genetically tractable.

There are two aspects that I plan to focus on with respect to the Nasonia genome. My research on honey bees focuses primarily on genes in higher order brain processing centers that are modulated by pheromones, and thereby may be involved in regulating the stereotyped changes in behavior that are produced by these pheromones. The genes that I have studied thus far are conserved in other insect species (such as mosquitos or Drosophila), and therefore may have similar functions. By studying these genes in Nasonia, I will have access to another Hymenopteran group, where the sequence and function will presumably be even more similar. Furthermore, Nasonia have three interbreeding species, whose courtship rituals seem to depend on pheromone perception; thus, QTL analysis of this pheromone perception will lead to other genes involved in brain processing of olfactory cues. Since the basic structure of the olfactory system is similar from insects to mammals, the information gleaned from these studies will be relevant in many species, and could lead to models regarding the mechanisms by which information is processed by the brain.

The second area that I am interested in involves chromatin-remodeling proteins, such as histone modifying and DNA-methylating proteins, which are involved in regulating gene expression and epigenetics. Such proteins play critical roles in many organismal and cellular processes, and have been shown to be involved in many human diseases, including leukemia, breast cancer, and Rett syndrome. These protein families have many members in humans, but the functions of only a handful are well understood. Previously, I cloned and characterized several of these enzymes in humans, and have committed to annotating these genes in the honey bee genome. I will annotate these genes in the Nasonia genome as well. Nasonia is a particularly interesting system in which to study these proteins, since there are many complex developmental and behavioral processes that are regulated by epigenetic mechanisms.

Thus, sequencing the Nasonia genome will provide exciting new resources for several invertebrate and vertebrate communities, and will facilitate the understanding of mechanisms of gene function at a variety of levels, including behavior, neural processing, development, and sex-determination.

Sincerely,

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